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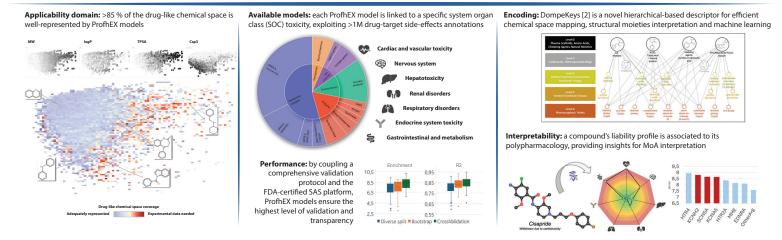
Access

## ProfhEX Al-driven platform enabling drug repurposing by in-silico polypharmacology estimations

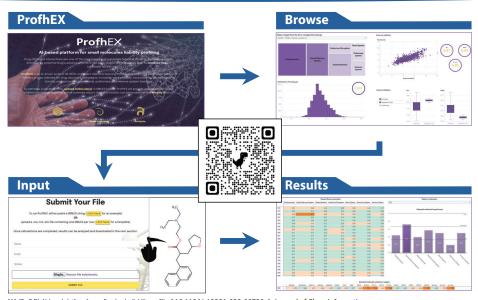
Filippo Lunghini<sup>1</sup>, Anna Fava<sup>1</sup>, Vincenzo Pisapia<sup>2</sup>, Francesco Sacco<sup>2</sup>, Daniela Iaconis<sup>1</sup> and Andrea Rosario Beccari<sup>1</sup> <sup>1</sup> EXSCALATE, Dompé Farmaceutici SpA, Via Tommaso de Amicis 95, 80123, Naples, Italy <sup>2</sup> Professional Service Department, SAS Institute, Via Darwin 20/22, 20143, Milan, Italy

Repurposing is a viable strategy for uncovering novel indications for already approved drugs, as they have the potential to synergistically interact with multiple targets. However, assessing a drug's pleiotropic effect is strongly limited by the scarcity of experimental evidence on drug-target interactions. In-silico simulations play an important role in supplementing missing experimental annotations: ProfhEX is a suite of AI-driven models capable of estimating potential interactions between drugs and therapeutically relevant targets, thereby proposing new drug repurposing strategies.

A first version of ProfhEX focusing on safety profiling has already been published [1], featuring >250K activity data over 46 targets. Models have been generated within the SASviya environment, leveraging state-of-the-art machine learning algorithms, chemistry-aware molecular descriptors "DompeKeys", consensus modelling, applicability domain, uncertainty evaluation and enhanced interpretability.



ProfhEX is freely available as webservice enabling high-throughput screening of molecules in a secure, code-free and intuitive cloud environment (https://profhex.exscalate.eu/)



**R4ALL Impact** 

ProfhEX provides estimations for drug-target interactions involving >600 therapeutically relevant targets, offering researchers a freely accessible tool for evaluating new drug repurposing hypotheses. Additionally, the platform can estimate >30 ADME endpoints and identify the most probable metabolic pathways, enabling comprehensive polypharmacological molecule profiling. Therefore, ProfhEX is well-suited to empower R4ALL activities through in-silico driven discovery of new mechanisms of action.

**Sas** 

😫 EXSCALATE 🛛 Dompé

"ProfhEX: Al-based platform for small molecules liability profiling", 10.1186/s13321-023-00728-6, Journal of Cheminformatics
"DompeKeys": a novel substructure-based descriptor for an efficient chemical space mapping and structural moieties interpretation in Machine Learning models, accepted paper, Journal of Cheminformatics